NCBI Entrez BLAST 2 sequences BLAST Example Help

# **BLAST 2 SEQUENCES**

This tool produces the alignment of two given sequences using <u>BLAST</u> engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from <u>NCBI ftp site</u> <u>Reference:</u> Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Parameters used in BLASTN program only:  Reward for a match:  Penalty for a mismatch:  Use Mega BLAST Strand option Not Applicable  Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter  Align  Sequence 1 Enter accession or GI or download from file or sequence in FASTA format from: 0 to: 0  Inqs snf gpm kgg nfg grs sgp ygg ggq yfa kpr ngg gy  Sequence 2 Enter accession or GI or download from file or sequence in FASTA format from: 0 to: 0  YDR RGR PGD GMV GFS ADE TWD SAI DTW SPS EWQ MAY  Align Clear Input	Program blastp ▼ Matrix BLOSUM62 ▼		· .	
Open gap 11 and extension gap 1 penalties gap x_dropoff 50 expect 10.0 word size 3 Filter  Align  Sequence 1 Enter accession or GI or download from file or sequence in FASTA format from: 0 to: 0  nqs snf gpm kgg nfg grs sqp ygg ggq yfa kpr nqg gy  Sequence 2 Enter accession or GI or download from file or sequence in FASTA format from: 0 to: 0  YDR RGR PGD GMV GFS ADE TWD SAI DTW SPS EWQ MAY	Parameters used in <u>BLASTN</u> program only:  Reward for a match: Penalty for a mismatch:		-	
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Comments and suggestions to <u>blast-help@ncbi.nlm.nih.gov</u>



# **Blast 2 Sequences results**

PubMed Entrez BLAST OMIM Taxonomy Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.5 [Nov-16-2002]** 

Matrix BLOSUM62 ▼ gap open: 11 gap extension: 1

x dropoff: 50 expect: 10.0 wordsize: 3 Filter ✓ Align

Sequence 1 lcl|seq\_1 Length 38

Sequence 2 lcl|seq\_2 Length 36

No significant similarity was found

# (FILE 'HOME' ENTERED AT 13:41:15 ON 12 JUN 2003)

#### FILE 'MEDLINE' ENTERED AT 13:45:48 ON 12 JUN 2003

- L1 0 S NON-CLASSICAL NUCLEOAR LOCALIZATION SIGNAL
- L2 1 S NON-CLASSICAL NUCLEAR LOCALIZATION SIGNAL

FILE 'CAPLUS, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH' ENTERED AT 13:47:32

ON 12 JUN 2003

- L3 6 S L2
- L4 2 DUP REM L3 (4 DUPLICATES REMOVED)

## (FILE 'HOME' ENTERED AT 14:31:19 ON 12 JUN 2003)

### FILE 'MEDLINE' ENTERED AT 14:31:43 ON 12 JUN 2003

- L1 0 S STABLY TRANSFECTED AND SCAFFOLD AND NUCLEAR LOCALIZATION
- L2 10 S STABLY TRANSFECTED AND SCAFFOLD
- L3 17 S PLASMID AND EBNA-1 AND EPISOM? AND (STABLE OR STABLY)
- L4 8 S PLASMID AND LARGE T AND EPISOM? AND (STABLE OR STABLY)
- L5 326 S (STABLY OR STABLE) AND EPISOM?
- L6 37 S L5 AND (EBNA OR LARGE T)

=> file stnguide